Changes in population size through time are a function of births, deaths, immigration, and emigration. Population biologists have devoted a disproportionate amount of time to models that assume immigration and emigration are non-existent. However, modern thinking suggests that these effects are quite important. For example, metapopulation dynamics are not possible without immigration and emigration in the subpopulations. In today’s material, we will explore 2 models for marked animals that estimate emigration and immigration to a population, or group of populations. Although these models are complicated, they bring more biological reality to the analysis of population dynamics.

**Pollock’s Robust Design**


**Example Robust Design Data**

In the file

```
J:\CLASSES\FW663\EXERCISE.17\robust.inp
```

is a set of robust design data. There are 5 trapping sessions with lengths of 2, 2, 4, 5, and 2, giving 15 total occasions. Only one group is present. No individual covariates are included. Work with these data enough to get a feel for the parameters of this complex model, and also the confounding of the emigration and immigration parameters under the t model.

**Multi-strata Model for Live Recaptures**

The multi-strata model of Brownie et al. (1993) and Hestbeck et al. (1991) allows animals to move between strata with transition probabilities. These models are an extension of the Cormack-Jolly-Seber model (CJS) (Cormack 1964, Jolly 1965, Seber 1965) live recapture model extended to multiple areas or strata.

**Example Multi-Strata Data**

In the file

```
J:\CLASSES\FW663\EXERCISE.17\mssurv.inp
```

is a set of multi-strata data. There are 4 occasions and 3 strata, labeled A, B, and C. Only one group is present. No individual covariates are included.
Literature Cited


